

SEQUENCE LISTING

<110> Chiang, Lillian Wei-Ming

<120> NARC8 Programmed Cell
Death-Associated Molecule and Uses Thereof

<130> 35800/207197

<150> 09/692,785

<151> 2000-10-20

<150> 60/161,188

<151> 1999-10-22

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1507

<212> DNA

<213> Homo sapeins

<220>

<221> CDS

<222> (368)...(1261)

<400> 1

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tccgccgagc ctgcccgggt ccgggcgctt gtctatgggc accacgggga tccagccaag      180
gtcgtcgaaa ccgtaattcc tgggcacaca tggcagctca gaaatgttgc ctgacctact      240
ttgaggagat gatttgagcg aaacacccat tctagcctgg atgacatgaa catctccgtt      300
tggctttgtg cttagactca agaacctgga gctagctgct gtgagaggat cagatgtccg      360
tgtgaag atg ctg gcg gcc cct atc aat cca tct gac ata aat atg atc      409
Met Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile
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1

5

10

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caa gga aac tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac      457
Gln Gly Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn
15 20 25 30
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gaa ggt gtt gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg      505
Glu Gly Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu
35 40 45
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aag cca gga gac tgg gtg att cca gca aat gct ggt tta gga acc tgg      553
Lys Pro Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp
50 55 60
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cgg acc gag gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt      601
Arg Thr Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser
65 70 75
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gac atc cct ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca Asp Ile Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr 80 85 90	649
gcc tac agg atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct Ala Tyr Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser 95 100 105 110	697
gtc atc cag aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag Val Ile Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln 115 120 125	745
atc gcc gca gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga Ile Ala Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg 130 135 140	793
cct gat atc cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag Pro Asp Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu 145 150 155	841
cat gtc atc aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc His Val Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe 160 165 170	889
ttt aag gac atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg Phe Lys Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly 175 180 185 190	937
aaa agc tcc aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg Lys Ser Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met 195 200 205	985
gta acc tat ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc Val Thr Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser 210 215 220	1033
ctg ctc att ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag Leu Leu Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln 225 230 235	1081
tgg aag aag gat cac agt cca gac cag ttc aag gag ctg atc ctc aca Trp Lys Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr 240 245 250	1129
ctg tgc gat ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc Leu Cys Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser 255 260 265 270	1177
cag gtc ccg ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag Gln Val Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys 275 280 285	1225
ccc ttc ata tct tca aag cag att ctc acc atg tga tcatcccaaa Pro Phe Ile Ser Ser Lys Gln Ile Leu Thr Met * 290 295	1271

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agagctggag tgacatggga ggggagggcg atctgagggg ctgggtgcag gccctcagt 1331
tggggctccc accttcccc gactactgtt ctctctactg cctcttcccta ttaggaggat 1391
ggtgaagcca gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac 1451
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<210> 2
<211> 297
<212> PRT
<213> Homo sapiens

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Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly
 20          25          30
Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro
 35          40          45
Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr
 50          55          60
Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile
 65          70          75          80
Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr
 85          90          95
Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile
 100         105         110
Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala
 115         120         125
Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp
 130         135         140
Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val
 145         150         155         160
Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys
 165         170         175
Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser
 180         185         190
Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr
 195         200         205
Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu
 210         215         220
Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys
 225         230         235         240
Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys
 245         250         255
Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val
 260         265         270
Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe
 275         280         285
Ile Ser Ser Lys Gln Ile Leu Thr Met
 290         295

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<210> 3
<211> 894
<212> DNA
<213> Homo sapiens

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<400> 3
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agcaatgtga	ccgggctgaa	gccaggagac	tgggtgattc	cagcaaatgc	tggtttagga	180
acctggcgga	ccgaggtgtg	gttcagcgag	gaagcactga	tccaagttcc	gagtgacatc	240
cctcttcaga	gcgctgccac	cctgggtgtc	aatccctgca	cagcctacag	gatgttgatg	300
gatttcgagc	aactgcagcc	aggggattct	gtcatccaga	atgcatccaa	cagcggagtg	360
gggcaagcgg	tcatccagat	cgccgcagcc	ctgggcctaa	gaaccatcaa	tgtgggtccga	420
gacagacctg	atatccagaa	gctgagtgac	agactgaaga	gtctgggggc	tgagcatgtc	480
atcacagaag	aggagctaag	aaggcccga	atgaaaaact	tctttaagga	catgccccag	540
ccacggcttg	ctctcaactg	tgttggtggg	aaaagctcca	cagagctgct	gcggcagtta	600
gcgctgtggag	gaaccatggt	aacctatggg	gggatggcca	agcagcccgt	cgtagcctct	660
gtgagcctgc	tcatTTTTAA	ggatctcaaa	cttcgaggct	tttggttgct	ccagtgggaag	720
aaggatcaca	gtccagacca	gttcaaggag	ctgactctca	cactgtgcga	tctcatccgc	780
cgaggccagc	tcacagcccc	tgccctgtcc	caggtcccgc	tgcaggacta	ccagtctgcc	840
ttggaagcct	ccatgaagcc	cttcatatct	tcaaagcaga	ttctcaccat	gtga	894

<210> 4
 <211> 1380
 <212> DNA
 <213> Homo sapeins

<220>
 <221> CDS
 <222> (13)...(1134)

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		Met	Trp	Val	Cys	Ser	Thr	Leu	Trp	Arg	Val	Arg	Thr	Pro		
		1				5						10				
gcc	cgg	cag	tgg	cgg	ggg	ctg	ctc	cca	gct	tct	ggc	tgt	cac	gga	cct	99
Ala	Arg	Gln	Trp	Arg	Gly	Leu	Leu	Pro	Ala	Ser	Gly	Cys	His	Gly	Pro	
	15					20					25					
gcc	gcc	tcc	tcc	tac	tcc	gca	tcc	gcc	gag	cct	gcc	cgg	gtc	cgg	gcg	147
Ala	Ala	Ser	Ser	Tyr	Ser	Ala	Ser	Ala	Glu	Pro	Ala	Arg	Val	Arg	Ala	
	30					35				40					45	
ctt	gtc	tat	ggg	cac	cac	ggg	gat	cca	gcc	aag	gtc	gtc	gaa	ctc	aag	195
Leu	Val	Tyr	Gly	His	His	Gly	Asp	Pro	Ala	Lys	Val	Val	Glu	Leu	Lys	
				50				55						60		
aac	ctg	gag	cta	gct	gct	gtg	aga	gga	tca	gat	gtc	cgt	gtg	aag	atg	243
Asn	Leu	Glu	Leu	Ala	Ala	Val	Arg	Gly	Ser	Asp	Val	Arg	Val	Lys	Met	
			65					70						75		
ctg	gcg	gcc	cct	atc	aat	cca	tct	gac	ata	aat	atg	atc	caa	gga	aac	291
Leu	Ala	Ala	Pro	Ile	Asn	Pro	Ser	Asp	Ile	Asn	Met	Ile	Gln	Gly	Asn	
		80					85						90			
tac	gga	ctc	ctt	cct	gaa	ctg	cct	gct	gtt	gga	ggg	aac	gaa	ggt	gtt	339
Tyr	Gly	Leu	Leu	Pro	Glu	Leu	Pro	Ala	Val	Gly	Gly	Asn	Glu	Gly	Val	
	95						100				105					
gca	cag	gtg	gta	gcg	gtg	ggc	agc	aat	gtg	acc	ggg	ctg	aag	cca	gga	387
Ala	Gln	Val	Val	Ala	Val	Gly	Ser	Asn	Val	Thr	Gly	Leu	Lys	Pro	Gly	
	110				115					120					125	

gac tgg gtg att cca gca aat gct ggt tta gga acc tgg cgg acc gag	435
Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu	
130 135 140	
gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt gac atc cct	483
Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro	
145 150 155	
ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca gcc tac agg	531
Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg	
160 165 170	
atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct gtc atc cag	579
Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln	
175 180 185	
aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag atc gcc gca	627
Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala	
190 195 200 205	
gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga cct gat atc	675
Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile	
210 215 220	
cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag cat gtc atc	723
Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile	
225 230 235	
aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc ttt aag gac	771
Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp	
240 245 250	
atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg aaa agc tcc	819
Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser	
255 260 265	
aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg gta acc tat	867
Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr	
270 275 280 285	
ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc ctg ctc att	915
Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile	
290 295 300	
ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag tgg aag aag	963
Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys	
305 310 315	
gat cac agt cca gac cag ttc aag gag ctg atc ctc aca ctg tgc gat	1011
Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp	
320 325 330	
ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc cag gtc ccg	1059
Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro	
335 340 345	
ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag ccc ttc ata	1107

Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile
 350 355 360 365

tct tca aag cag att ctc acc atg tga tcaccccaaa agagctggag 1154
 Ser Ser Lys Gln Ile Leu Thr Met *
 370

tgacatggga ggggagggcg atctgagggg ctgggtgcag gcccctcagt tggggctccc 1214
 accttcccca gactactgtt ctctcactg cctcttcccta ttaggaggat ggtgaagcca 1274
 gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac tctcccttcc 1334
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1380

<210> 5
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 5
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 Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro Ala Ala Ser
 20 25 30
 Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Ala Leu Val Tyr
 35 40 45
 Gly His Gly Asp Pro Ala Lys Val Val Glu Leu Lys Asn Leu Glu
 50 55 60
 Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met Leu Ala Ala
 65 70 75 80
 Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn Tyr Gly Leu
 85 90 95
 Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val Ala Gln Val
 100 105 110
 Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly Asp Trp Val
 115 120 125
 Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu Ala Val Phe
 130 135 140
 Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro Leu Gln Ser
 145 150 155 160
 Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg Met Leu Met
 165 170 175
 Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln Asn Ala Ser
 180 185 190
 Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala Ala Leu Gly
 195 200 205
 Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile Gln Lys Leu
 210 215 220
 Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile Thr Glu Glu
 225 230 235 240
 Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp Met Pro Gln
 245 250 255
 Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser Thr Glu Leu
 260 265 270
 Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr Gly Gly Met
 275 280 285
 Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile Phe Lys Asp
 290 295 300
 Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys Asp His Ser

305 310 315 320
 Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp Leu Ile Arg
 325 330 335
 Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro Leu Gln Asp
 340 345 350
 Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile Ser Ser Lys
 355 360 365
 Gln Ile Leu Thr Met
 370

<210> 6
 <211> 1122
 <212> DNA
 <213> Homo sapeins

<400> 6
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 gcccgggtcc gggcgcttgt ctatgggcac cagggggatc cagccaaggt cgtcgaactc 180
 aagaacctgg agctagctgc tgtgagagga tcagatgtcc gtgtgaagat gctggcggcc 240
 cctatcaatc catctgacat aaatatgata caaggaaact acggactcct tcctgaactg 300
 cctgctgttg gaggaacga aggtgttgca caggtggtag cgggtggcag caatgtgacc 360
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 gaggtgtgtg tcagcgagga agcactgata caagttccga gtgacatccc tcttcagagc 480
 gctgccaccc tgggtgtcaa tccctgcaca gcctacagga tgttgatgga tttcgagcaa 540
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 atccagatcg ccgcagccct gggcctaaga accatcaatg tggtcagaga cagacctgat 660
 atccagaagc tgagtgcagc actgaagagt ctgggggctg agcatgtcat cacagaagag 720
 gagctaagaa ggcccgaat gaaaaacttc tttaaggaca tgccccagcc acggcttgct 780
 ctcaactgtg ttggtgggaa aagctccaca gagctgctgc ggcagttagc gcgtggagga 840
 accatggtaa cctatggggg gatggccaag cagcccgtcg tagcctctgt gagcctgctc 900
 atttttaagg atctcaact tcgaggcttt tggttgtccc agtggaagaa ggatcacagt 960
 ccagaccagt tcaaggagct gatcctcaca ctgtgcgata tcatccgccg aggccagctc 1020
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<210> 7
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zinc-binding dehydrogenase consensus sequence

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 20 25 30
 Ile Tyr Lys Gly Gly Leu Gly Leu Met Tyr Pro Gly Pro Gly Asp Gly
 35 40 45
 Thr His Leu Phe Pro Val Lys Leu Pro Leu Val Leu Gly His Glu Gly
 50 55 60
 Ala Gly Val Val Glu Glu Val Gly Ser Gly Val Thr Gly Phe Lys Leu
 65 70 75 80
 Lys Val Gly Lys Phe Lys Val Gly Asp Arg Val Val Val Leu Pro Leu
 85 90 95

Val	Gly	Cys	Cys	Gly	Arg	Gly	Ser	Ala	Glu	Cys	Glu	Phe	Cys	Lys	Gly	
			100					105					110			
Ser	Gly	Arg	Glu	Asn	Leu	Cys	Pro	Lys	Gly	Arg	Ala	Thr	Gly	Pro	Gly	
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Lys	Gly	Leu	Met	Pro	Asn	Asp	Gly	Phe	Gly	Gly	Phe	Thr	Pro	Lys	Lys	
	130					135					140					
Gln	Gly	Ala	Pro	Cys	Lys	Gly	Lys	Asp	Gly	Tyr	His	Phe	Met	Gly	Asp	
145					150					155					160	
Gly	Gly	Phe	Ala	Glu	Tyr	Val	Val	Val	Pro	Ala	Arg	Arg	Asn	Asp	Tyr	
				165					170					175		
Phe	Val	Val	Lys	Ile	Pro	Asp	Gly	Leu	Asp	Asp	Glu	Ile	Pro	Leu	Glu	
			180					185					190			
Glu	Ala	Glu	Ala	Ala	Ala	Leu	Leu	Gly	Cys	Ala	Gly	Leu	Thr	Ala	Tyr	
	195						200					205				
Gly	Ala	Leu	Val	Arg	Ala	Ala	Lys	Val	Gly	Ser	Leu	Pro	Pro	Gly	Asp	
	210					215					220					
Thr	Val	Leu	Val	His	Gly	Ala	Gly	Gly	Gly	Val	Gly	Leu	Ala	Ala	Val	
225					230					235					240	
Gln	Leu	Ala	Lys	Ala	Ala	Gly	Ala	Ala	Arg	Val	Ile	Ala	Val	Asp	Ser	
			245						250					255		
Ser	Glu	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Lys	Glu	Leu	Gly	Ala	Asp	Leu	
	260							265					270			
Asp	Ala	Asp	Phe	Val	Asn	Asn	Ser	Lys	Gly	Leu	Pro	Thr	Val	Asn	Asp	
	275						280					285				
Asp	Arg	Lys	Glu	Asp	Phe	Val	Glu	Ala	Ile	Lys	Glu	Leu	Thr	Gly	Gly	
	290					295					300					
Arg	Asn	Gly	Ala	Gly	Gly	Val	Asp	Val	Val	Leu	Asp	Cys	Val	Gly	Ile	
305					310					315					320	
Gly	Leu	Gly	Gly	Ala	Thr	Leu	Asp	Ala	Ala	Leu	Ala	Leu	Leu	Lys	Pro	
				325					330					335		
Gly	Gly	Arg	Leu	Val	Val	Val	Gly	Pro	Lys	Val	Ala	Val	Gly	Val	Pro	
			340					345					350			
Gly	Gly	Gly	Ala	Pro	Ile	Pro	Leu	Leu	Leu	Leu	Lys	Glu	Glu	Glu	Lys	
	355						360					365				
Leu	Tyr	Glu	Arg	Ser	Ile	Lys	Gly	Ser	Phe	Leu	Gly	Gly	Arg	Lys	Pro	
	370					375					380					
Arg	Leu	Ser	Val	Leu	Ser	Val	Asp	Thr	Thr	Pro	Asp	Glu	Leu	Arg	Glu	
385					390					395					400	
Ala	Leu	Asp	Leu	Leu	Ala	Ser	Gly	Ile	Lys	Asp	Lys	Asn	Gly	Lys	Gly	
				405					410					415		
Val	Leu	Asp	Pro	Leu	Ile	Thr	His	Thr	Leu	Pro	Pro	Leu	Asp	Asp	Ser	
			420					425					430			
Leu	Glu	Glu	Ala	Asn	Glu	Ala	Phe	Glu	Leu	Leu	Glu	Ser	Gly	Lys	His	
	435						440					445				
Gly	Lys	Val	Val	Leu	Ile	Pro										
	450					455										